

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/828,323DATE: 09/16/97
TIME: 09:40:04

INPUT SET: S20352.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

#7
9/26/97
JZ

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: O'Donnell, Michael
6
7 (ii) TITLE OF INVENTION: DNA POLYMERASE III HOLOENZYME
8
9 (iii) NUMBER OF SEQUENCES: 60
10
11 (iv) CORRESPONDENCE ADDRESS:
12 (A) ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
13 (B) STREET: Clinton Square, P.O. Box 1051
14 (C) CITY: Rochester
15 (D) STATE: New York
16 (E) COUNTRY: U.S.A.
17 (F) ZIP: 14603
18
19 (v) COMPUTER READABLE FORM:
20 (A) MEDIUM TYPE: Floppy disk
21 (B) COMPUTER: IBM PC compatible
22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
23 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
24
25 (vi) CURRENT APPLICATION DATA:
26 (A) APPLICATION NUMBER: US 08/828,323
27 (B) FILING DATE: 28-MAR-1997
28 (C) CLASSIFICATION:
29
30 (viii) ATTORNEY/AGENT INFORMATION:
31 (A) NAME: Goldman, Michael L.
32 (B) REGISTRATION NUMBER: 30,727
33 (C) REFERENCE/DOCKET NUMBER: 19603/10213
34
35 (ix) TELECOMMUNICATION INFORMATION:
36 (A) TELEPHONE: (716) 263-1304
37 (B) TELEFAX: (716) 263-1600
38
39
40 (2) INFORMATION FOR SEQ ID NO:1:
41
42 (i) SEQUENCE CHARACTERISTICS:
43 (A) LENGTH: 28 amino acids
44 (B) TYPE: amino acid
45 (C) STRANDEDNESS: single
46 (D) TOPOLOGY: linear

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47
48 (ii) MOLECULE TYPE: peptide
49
50
51
52
53 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
54
55 Met Leu Arg Leu Tyr Pro Glu Gln Leu Arg Ala Gln Leu Asn Glu Gly
56 1 5 10 15
57
58 Leu Arg Ala Ala Tyr Leu Leu Leu Gly Asn Asp Pro
59 20 25
60
61 (2) INFORMATION FOR SEQ ID NO:2:
62
63 (i) SEQUENCE CHARACTERISTICS:
64 (A) LENGTH: 21 amino acids
65 (B) TYPE: amino acid
66 (C) STRANDEDNESS: single
67 (D) TOPOLOGY: linear
68
69 (ii) MOLECULE TYPE: peptide
70
71
72
73
74 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
75
76 Ala Ala Tyr Leu Leu Leu Gly Asn Asp Pro Leu Leu Leu Gln Glu Ser
77 1 5 10 15
78
79 Gln Asp Ala Val Arg
80 20
81
82 (2) INFORMATION FOR SEQ ID NO:3:
83
84 (i) SEQUENCE CHARACTERISTICS:
85 (A) LENGTH: 14 amino acids
86 (B) TYPE: amino acid
87 (C) STRANDEDNESS: single
88 (D) TOPOLOGY: linear
89
90 (ii) MOLECULE TYPE: peptide
91
92
93
94
95 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
96
97 Ala Gln Glu Asn Ala Ala Trp Phe Thr Ala Leu Ala Asn Arg
98 1 5 10
99

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100 (2) INFORMATION FOR SEQ ID NO:4:

101

102 (i) SEQUENCE CHARACTERISTICS:

103 (A) LENGTH: 24 amino acids

104 (B) TYPE: amino acid

105 (C) STRANDEDNESS: single

106 (D) TOPOLOGY: linear

107

108 (ii) MOLECULE TYPE: peptide

109

110

111

112

113 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

114

115 Val Glu Gln Ala Val Asn Asp Ala Ala His Phe Thr Pro Phe His Trp

116 1 5 10 15

117

118 Val Asp Ala Leu Leu Met Gly Lys

119 20

120

121 (2) INFORMATION FOR SEQ ID NO:5:

122

123 (i) SEQUENCE CHARACTERISTICS:

124 (A) LENGTH: 33 base pairs

125 (B) TYPE: nucleic acid

126 (C) STRANDEDNESS: single

127 (D) TOPOLOGY: linear

128

129 (ii) MOLECULE TYPE: DNA (genomic)

130

131

132

133

134 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

135

136 GTACAACCGA ATCATATGTT ACCCAGCGAG CTC

137

33

138 (2) INFORMATION FOR SEQ ID NO:6:

139

140 (i) SEQUENCE CHARACTERISTICS:

141 (A) LENGTH: 1032 base pairs

142 (B) TYPE: nucleic acid

143 (C) STRANDEDNESS: single

144 (D) TOPOLOGY: linear

145

146 (ii) MOLECULE TYPE: DNA (genomic)

147

148

149

150

151 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

152

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153	ATGATTCCGGT TGTACCCGGA ACAACTCCGC GCGCAGCTCA ATGAAGGGCT GCGCGCGGCG	60
154		
155	TATCTTTTAC TTGGTAACGA TCCTCTGTTA TTGCAGGAAA GCCAGGACGC TGTTCGTCAG	120
156		
157	GTAGCTGCGG CACAAGGATT CGAAGAACAC CACACTTTTT CCATTGATCC CAACACTGAC	180
158		
159	TGGAATGCGA TCTTTTCGTT ATGCCAGGCT ATGAGTCTGT TTGCCAGTCG ACAAACGCTA	240
160		
161	TTGCTGTTGT TACCAGAAAA CGGACCGAAT GCGGCGATCA ATGAGCAACT TCTCACACTC	300
162		
163	ACCGGACTTC TGCATGACGA CCTGCTGTTG ATCGTCCGCG GTAATAAATT AAGCAAAGCG	360
164		
165	CAAGAAAATG CCGCCTGGTT TACTGCGCTT GCGAATCGCA GCGTGCAGGT GACCTGTCAG	420
166		
167	ACACCGGAGC AGGCTCAGCT TCCCCGCTGG GTTGCTGCGC GCGCAAAACA GCTCAACTTA	480
168		
169	GAAC TGGATG ACGCGGCAAA TCAGGTGCTC TGCTACTGTT ATGAAGGTAA CCTGCTGGCG	540
170		
171	CTGGCTCAGG CACTGGAGCG TTTATCGCTG CTCTGGCCAG ACGGCAAATT GACATTACCG	600
172		
173	CGCGTTGAAC AGGCGGTGAA TGATGCCGCG CATTTACCCC CTTTTCATTG GGTGATGCT	660
174		
175	TTGTTGATGG GAAAAAGTAA GCGCGCATTG CATATTCTTC AGCAACTGCG TCTGGAAGGC	720
176		
177	AGCGAACCGG TTATTTTGTT GCGCACATTA CAACGTGAAC TGTTGTTACT GGTAAACCTG	780
178		
179	AAACGCCAGT CTGCCCATAC GCCACTGCGT GCGTTGTTTG ATAAGCATCG GGTATGGCAG	840
180		
181	AACCGCCGGG GCATGATGGG CGAGGCGTTA AATCGCTTAA GTCAGACGCA GTTACGTCAG	900
182		
183	GCCGTGCAAC TCCTGACACG AACGGAACTC ACCCTCAAAC AAGATTACGG TCAGTCAGTG	960
184		
185	TGGGCAGAGC TGGAAGGGTT ATCTCTTCTG TTGTGCCATA AACCCCTGGC GGACGTATTT	1020
186		
187	ATCGACGGTT GA	1032

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

204	CCGAACAGCT GATTCGTAAG CTGCCAAGCA TCCGTGCTGC GGATATTCGT TCCGACGAAG	60
205		

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206 AACAGACGTC GACCACAACG GATACTCCGG CAACGCCTGC ACGCGTCTCC ACCACGCTGG 120
207
208 GTAAGTCTG 127
209
210 (2) INFORMATION FOR SEQ ID NO:8:
211
212 (i) SEQUENCE CHARACTERISTICS:
213 (A) LENGTH: 102 base pairs
214 (B) TYPE: nucleic acid
215 (C) STRANDEDNESS: single
216 (D) TOPOLOGY: linear
217
218 (ii) MOLECULE TYPE: DNA (genomic)
219
220
221
222
223 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
224
225 TATGAAATCT TTACAGGCTC TGTTTGGCGG CACCTTTGAT CCGGTGCACT ATGGTCATCT 60
226
227 AAAACCCGTT GGAAGCGTGG CCGAAGTTTT GATTGGTCTG AC 102
228
229 (2) INFORMATION FOR SEQ ID NO:9:
230
231 (i) SEQUENCE CHARACTERISTICS:
232 (A) LENGTH: 343 amino acids
233 (B) TYPE: amino acid
234 (C) STRANDEDNESS: single
235 (D) TOPOLOGY: linear
236
237 (ii) MOLECULE TYPE: peptide
238
239
240
241
242 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
243
244 Met Ile Arg Leu Tyr Pro Glu Gln Leu Arg Ala Gln Leu Asn Glu Gly
245 1 5 10 15
246
247 Leu Arg Ala Ala Tyr Leu Leu Leu Gly Asn Asp Pro Leu Leu Leu Gln
248 20 25 30
249
250 Glu Ser Gln Asp Ala Val Arg Gln Val Ala Ala Ala Gln Gly Phe Glu
251 35 40 45
252
253 Glu His His Thr Phe Ser Ile Asp Pro Asn Thr Asp Trp Asn Ala Ile
254 50 55 60
255
256 Phe Ser Leu Cys Gln Ala Met Ser Leu Phe Ala Ser Arg Gln Thr Leu
257 65 70 75 80
258

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SEQUENCE VERIFICATION REPORT
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Original Text